AN ADDITION TO THE RAINBOWFISH (MELANOTAENIIDAE) FAUNA OF NORTH QUEENSLAND

KATRINA L. McGUIGAN

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A new Melanotaeniid species is described from 28 specimens collected from the Johnstone River, north Queensland. *Melanotaenia utcheensis* sp. nov. was found in sites with moderate to high water flow over cobbles and boulders and all sites are in close proximity to major agricultural activity and have moderately to highly disturbed riparian vegetation. *Melanotaenia utcheensis* sp. nov. has a distinctive colour pattern with a blue-black mid-lateral band and orange margins on vertical scale rows. It is morphologically distinct from the broadly sympatric *Melanotaenia eachamensis* (Allen & Cross, 1982) and *Melanotaenia splendida splendida* (Peters, 1866), as well as from its sister species from southern Queensland/northern New South Wales, *Melanotaenia duboulayi* (Castelnau, 1878). In particular, *M. utcheensis* sp. nov. has more first dorsal spines and fewer vertical scale rows and anal rays than *M. s. splendida*, and fewer soft second dorsal rays and more pectoral rays than either *M. eachamensis* or *M. duboulayi*. The new species is also generally smaller than either *M. s. splendida* or *M. eachamensis* and intermediate between them in eye diameter, predorsal length, head depth and body depth. ❐ *Melanotaeniidae, Melanotaenia, rainbowfish, freshwater, North Queensland, Johnstone River.*

K.L. McGuigan, Department of Zoology and Entomology, The University of Queensland, St Lucia 4072, Australia (e-mail: kmcguigan@zen.uq.edu.au); 10 May 2001.

The family Melanotaeniidae is endemic to freshwaters of Australia and New Guinea. These small rainbowfish (usually less than 12cm standard length) tend to be locally abundant, representing a major component of the freshwater fauna of the region. Rainbowfish are also popular in the aquarium trade both in Australia and overseas. There are currently 68 described Melanotaeniidae species in seven genera (Allen & Renyaan, 1998). Recent changes to taxonomy have primarily resulted from surveys in New Guinea, where fifteen species and one genus have been described since 1990 (see Allen & Renyaan, 1998). In Australia there are 4 genera with 13 species, a number that has remained static since Crowley et al. (1986) reassessed the status of southern *Melanotaenia*. *Melanotaenia* is the numerically dominant genus in Australia where it is represented by ten described species and 4 subspecies.

Some *Melanotaenia* species are geographically restricted while others are widespread, occupying a range of habitats. Widespread taxa often display interpopulation variation in morphology and colouration, making classification difficult. Intraspecific phenotypic variation is recognised in the aquarium trade where rainbowfish are sold as types, usually named for the collection locality. *Melanotaenia splendida splendida* (Peters, 1866) is one such widespread taxon (Cape York Peninsula to Gladstone) that is sold as several types due to variation among populations in both colour and morphology.

The high level of intraspecific variation in *M. s. splendida* has caused confusion over the status of the geographically restricted and poorly characterised *Melanotaenia eachamensis* (Allen & Cross, 1982) (Crowley & Ivantsoff, 1991; Zhu et al., 1994, 1998; Pusey et al., 1997). Pusey et al.'s (1997) study of morphological variation of rainbowfish in the region supported separate species status for *M. eachamensis*. Mapping the distribution of and determining the relationship among mtDNA lineages on the Atherton Tablelands confirmed the species status of *M. eachamensis* (Zhu et al., 1994, 1998). Several of the *M. eachamensis* populations identified by Pusey et al. (1997) represented new lower altitudinal limits for the species (Rankin, Fisher and Utchee Creeks). However, subsequent mtDNA analysis of fish from those sites indicated that they represented a distinct lineage, more closely related to the southern species, *Melanotaenia duboulayi* (Castelnau, 1878) and *M. fluviatilis* (Castelnau, 1878) than to *M. eachamensis* (McGuigan et al., 2000: fig. 1). MtDNA analysis of high altitude populations not

previously characterised for morphology revealed another unique lineage, closely related to that observed in Rankin, Fisher and Utchee Creeks (McGuigan et al., 2000: fig. 1). These lineages exhibit divergences from described species consistent with a cessation of gene flow between one and two myr ago (McGuigan et al., 2000).

The status of the Utchee Creek population has been debated previously. It is sold in the aquarium trade as the Utchee Creek Type. Leggett & Merrick (1987) considered the population to be banded rainbowfish (*Melanotaenia trifasciata* Rendahl, 1922), which they resemble in colour pattern. Allen & Cross (1982) identified fish from Utchee Creek as a population of *M. s. splendida* with unusual colouration but conceded the possibility that they represented an undescribed species. In his rainbowfish classification scheme Schmida (1997) distinguished the Utchee Creek Type from all described species and, as did McGuigan et al. (2000), placed it in a group containing *M. eachamensis*, *M. duboulayi* and *M. fluviatilis*, along with *M. s. australis* populations from Western Australia.

This paper describes *M. utcheensis* sp. nov. from Utchee, Fisher and Short Creeks in the Johnstone River, north Queensland. The new species is compared to the broadly sympatric *M. eachamensis* and *M. s. splendida* and also to its sister species, *M. duboulayi*.

MATERIALS AND METHODS

SPECIMEN COLLECTION. *Melanotaenia eachamensis*, *M. s. splendida* and *M. utcheensis* sp. nov. were collected during 1998 and 1999 from sites in northeast Queensland (Fig. 2) using dip nets and traps. *Melanotaenia duboulayi* were collected in the same manner from Kholo Creek (Brisbane River) and Amamoor Creek (Mary River) in southeast Queensland (Fig. 2). Information on land use, riparian vegetation, substrate, and channel characteristics was collected at each site. Fish were transported to The University of Queensland, Brisbane and held in 72L tanks at 26°C until processing.

MORPHOLOGICAL CHARACTERISATION. The definition of characters and the format of the description follows Allen & Renyaan (1998). Morphological characterisation was performed on anaesthetised live fish (1:10000 MS222, Sigma Chemical Company). Fin ray and scale row counts were made using a light microscope. Morphometric measurements were made on microscope images using Video Trace (Leading Edge Pty Ltd, 1994); a program that facilitates calibrated measurement directly from a live video feed. Type specimens were then euthanased by anaesthetic overdose and deposited at the Queensland Museum.

Data analysis was conducted using SPSS for Windows v. 9 (SPSS Inc., 1999). Meristic data was non-normally distributed, and could not be normalised through standard transformations. A Kruskall-Wallace test was conducted on all meristic variables and the sequential Bonferroni technique (Rice, 1989: $\propto$=0.05, k=7) used to control for group-wide type-I error. Variables that remained significant after correction were subject to a non-parametric multiple comparison test with unequal sample sizes (Zar, 1984) to determine whether the significant result was due to *M. utcheensis* sp. nov. The same technique was used to assess the meristic similarity of *M. eachamensis* and *M. s. splendida*.

Morphometric data was natural log transformed. To allow comparison of shape without the confounding effect of size (as indexed by standard length) data were size corrected using the formula:

$$\text{scaled variable} = \text{observed variable} \times \left(\frac{\text{set standard length}}{\text{observed standard length}} \right)^{b}$$

where b was the slope of the regression (specific for sex within population) of the observed variable on standard length; set standard length was 4.0 (=ln 55mm) as this value fell within the range of all species.

A discriminant functions analysis (DFA) was conducted on the size-corrected data with species as the discriminator. A one-way ANOVA with planned comparisons was used to compare the discriminant scores of *M. utcheensis* sp. nov. with all other species. A one-way ANOVA with planned comparisons was also used to compare *M. utcheensis* sp. nov. with all other species for univariate morphometric variables. Again, the morphological similarity between *M. eachamensis* and *M. s. splendida* was determined in the same way.

Melanotaenia utcheensis sp. nov.
(Fig. 3)

ETYMOLOGY. Named for the type locality, Utchee Creek, and in recognition of the history in the aquarium trade of the Utchee Creek Type.

MATERIAL. HOLOTYPE: QM I32159, ♂, Utchee Creek, North Johnstone R. (17°38'30"S 145°56'20"E). PARATYPES: Utchee Creek, North Johnstone R. (17°38'30"S 145°56'20"E), 5 females, QM I32160-32164 inclusive; Fisher Creek, North Johnstone R. (17°34'55"S 145°53'55"E), 2 males, QM I32165 and 32166, 5 females, QM I32167-32171 inclusive; Short Creek, North Johnstone R. (17°23'00"S 145°40'00"E), 10 males, QM I32172 and 5 females, QM I32173.

DESCRIPTION. The value of the holotype is presented with the observed paratypic range in parentheses. Dorsal rays VII-I,12 (V to VII-I, 10 to 12); anal rays I,19 (I, 16 to 20); pectoral rays 12 (11 to 15); horizontal scale rows 10 (9 to 11); vertical scale rows 34 (32 to 35); predorsal scales 13 (13-16).

Greatest body depth 34mm (31-38), head length 36mm (34-42) both as a proportion of standard length. Greatest body width 24mm (17-28) as a proportion of body depth. Snout length 32mm (34-43), eye diameter 28mm (24-32), interorbital width 22mm (19-28), depth of caudal peduncle 25mm (20-30), length of caudal peduncle 17mm (11-18) as proportions of head length.

Upper and lower jaws are of approximately equal length, oblique with a typically abrupt bend in the premaxilla between the anterior horizontal and lateral portions; the maxilla ends in front of the anterior edge of the eye; lips are thin. Scales are arranged in regular horizontal rows and their posterior edge is slightly crenulate; predorsal scales extend to the posterior end of the interorbital; preopercle has 2 scale rows from the posterior angle to the edge of the eye.

The origin of the first dorsal fin is anterior to the anal fin origin. The depressed longest first dorsal ray (second or third from origin) reaches half way between the insertion of the first dorsal and the origin of the second dorsal in females and ranges in males from the spine to the fourth soft ray of the second dorsal. The second dorsal fin origin is posterior to the anal fin origin. When depressed the longest rays of the second dorsal fin (usually second or third from insertion) extend just past the point of insertion in females, but reach almost to the caudal fin in males. The longest rays of the anal fin (usually second or third from insertion) have a depressed length the same as those of the second dorsal. In males both the second dorsal and anal fins are elongated and show a boxy outline when extended, whereas in females the fins are rounded, giving them a more ovaloid outline when extended. Length of pelvic fins is 18mm (15-26), pectoral fins 21mm (13-19) and caudal fin 17mm (8-19), all as a proportion of head length. The pelvic fin extends half to two-thirds of the way to the anal fin origin in females and smaller males, but reaches to the third anal soft ray in large males. Pectoral fins are rounded. The caudal fin is moderately forked.

TABLE 1. Structure matrix from the discriminant functions analysis. Superscripts denote loading rank for the 3 variables that contribute most to that function, ranging from highest loading (1) to third highest (3).

	DF1	DF2	DF3
Snout Length	-0.026	0.544^{3}	0.749^{1}
Eye Diameter	0.371^{3}	0.019	0.338^{2}
Head Length	-0.079	0.266	0.149
Predorsal Length	0.289	0.672^{1}	0.177^{1}
Head Depth	-0.618^{1}	0.268	0.061
Body Depth	-0.469^{2}	0.589^{2}	-0.104

Colour in Life. The overall body colour is silver, often with an orange cast near the midline. The head and gill region is silver to pink and fish often have an obvious reddish cheek patch. Scales tend towards purple iridescence, especially on the upper half of the body. There is an obvious orange stripe between horizontal scale rows. A typical *Melanotaenia* mid-lateral band starts dark at the tail and fades forwards, tending towards blue in males and black in females. Anal, dorsal, pelvic and caudal fins range from translucent to deep red, being most strongly pigmented in males. Anal, second dorsal and pelvic fins often have black margins, especially in males. Pectoral fins are translucent.

Colour in Alcohol. The underside is pale, generally tawny in colour. Above the mid-lateral line scales are outlined in grey, with blue tones in some specimens. Fins retain black margins, but the red in anal and dorsal fins fades to pink. Dark mid-lateral bands are retained.

Sexual Dimorphism. ♂♂ and ♀♀ are easily distinguished on the basis of external characteristics. ♂♂ tend to be more strongly pigmented than ♀♀. ♂♂ are also deeper bodied. As described above, ♂♂ have longer pelvic, dorsal and anal fins. The outline of extended second dorsal and anal fins is distinctively boxy in ♂♂ and ovaloid in ♀♀.

COMPARISONS. *Melanotaenia utcheensis* can be discriminated from *M. eachamensis*, *M. s. splendida* and *M. duboulayi* on the basis of multivariate morphology (Fig. 4). *M. utcheensis* differs from all other species on Discriminant

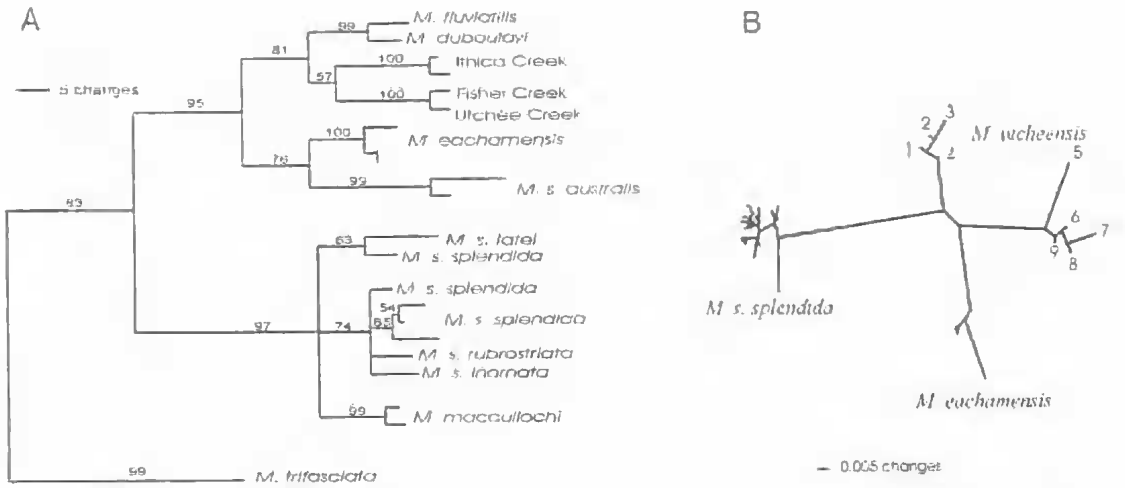

FIG. 1. A, Maximum parsimony phylogeny of mtDNA cytochrome b (351 bp) and control region (331 bp) sequence, adapted from McGuigan et al. (2000). Bootstrap support for nodes are indicated above branches. *M. utcheensis* sp. nov. represented by sequences from Ithica, Utchee and Fisher Creeks. B, Neighbour-joining network of mtDNA control region sequence (331 bp) (McGuigan & Moritz, unpubl.). Geographic locations of the nine *M. utcheensis* alleles are: 1, North Johnstone R. below the Malanda Falls; 2, Bromfield Swamp, North Johnstone R. below Malanda Falls and Ithica R.; 3, Ithica R.; 4, Ithica R.; 5, Gillies Creek; 6, Utchee Creek; 7, unnamed tributary of North Johnstone R., near Glenn Allyn; 8, Rankin, Fisher, Tregothanana and Utchee Creeks; 9, Utchee Creek.

Functions 1 (DF1) and 3 (DF3), but is distinct from only *M. duboulayi* on DF2 (one-way ANOVA with planned comparisons: $p<0.001$ for all significant comparisons) (Fig. 4). Factor loadings indicate that negative contributions from depth variables and positive contributions from length variables dominate DF1 (Table 1). *M. eachamensis* has low scores on DF1 due to its deep body and head, and small eyes and across DF1 species are progressively shallower in head and body, and larger eyed, with *M. s. splendida* at the extreme of this trend (Fig. 4; Table 2). DF2 is determined by positive contributions from all traits (Table 1) and *M. duboulayi* is distinct on DF2 because it is generally shorter and shallower than other species (Fig. 4; Table 2). DF3 is dominated by positive contributions from snout length and eye diameter, with *M. utcheensis* having short snouts and small eyes (Table 2; Fig. 4).

Melanotaenia utcheensis was observed to be morphologically most similar to the southern species *M. duboulayi* (Table 2). This supports the mtDNA sequence data, which indicates that they are sister species (Fig. 1). *Melanotaenia utcheensis* differs from *M. duboulayi* in having fewer soft second dorsal rays and more pectoral rays, as well as a longer predorsal distance and a deeper maximum body depth (Tables 2 and 3). *Melanotaenia utcheensis* is more distinct from its sympatric congeners *M. eachamensis* and *M. s. splendida*, differing in most of the traits measured (Tables 2 and 3). *Melanotaenia utcheensis* has fewer vertical scale rows, anal rays, and first dorsal spines than *M. s. splendida*; fewer second dorsal rays and more pectoral rays than *M. eachamensis* (Tables 2 and 3). Standard length, snout length, head length and depth, and body depth of *M. utcheensis* are less than that of *M. eachamensis*, but eye diameter is greater (Table 2). Compared to *M. s. splendida*, *M. utcheensis* has a shorter standard length, snout length, eye diameter, predorsal length and head depth, but a deeper body (Table 2). *Melanotaenia eachamensis* differs from *M. s. splendida* in having fewer vertical scale rows and anal rays, more first dorsal spines and second dorsal rays, and being shorter in standard length and predorsal length, having smaller eyes and a deeper head and body (Tables 2, 3). The intermediate position of *M. utcheensis* between *M. eachamensis* and *M. s. splendida* in both multivariate morphospace (Fig. 4) and in univariate traits (Table 2) probably contributed to the lack of previous recognition of species status.

Morphometric analyses of rainbowfish species by McGuigan et al. (2000) suggested that some characters particularly reflect phylogenetic history, while others reflect local adaptation,

TABLE 2. Mean meristic and morphometric measurement (mm) ± standard error. All morphometric measurements (except standard length) are corrected for standard length (see equation in text). Asterix (*) indicates a significant difference between *M. utcheensis* and the asterixed species; hash (#) inicates a significant difference between *M. eachamensis* and *M. s. splendia* at $p<0.05$ significance level (from one-way ANOVA with planned comparisons for size-corrected morphometric data and from nonparametric multiple comparisons for merisitc data; see text for details).

	M. utcheensis (53)	*M. eachamensis* (90)	*M. s. splendida* (25)	*M. duboulayi* (40)
Vertical Scale Rows	31.72 ± 0.27	31.67 ± 0.15#	33.00 ± 0.13*	32.95 ± 0.19
Horizontal Scale Rows	9.87 ± 0.08	10.17 ± 0.06	10.00 ± 0.06	10.25 ± 0.08
Anal Rays	18.79 ± 0.14	18.80 ± 0.14#	20.12 ± 0.22*	18.73 ± 0.17
1st Dorsal Spines	5.40 ± 0.11	5.42 ± 0.08#	4.88 ± 0.12*	4.95 ± 0.12
2nd Dorsal Rays	10.79 ± 0.09	11.91 ± 0.12*#	10.72 ± 0.17	11.43 ± 0.24*
Pelvic Rays	5.96 ± 0.04	6.02 ± 0.04	5.00 ± 0.00	6.00 ± 0.00
Pectoral Rays	12.62 ± 0.14	11.90 ± 0.08*	12.00 ± 0.11	11.48 ± 0.11*
Standard Length	46.02 ± 0.74	51.28 ± 0.76*#	56.36 ± 1.90*	46.18 ± 0.88
Snout Length	3.24 ± 0.05	3.62 ± 0.05*	3.73 ± 0.11*	3.10 ± 0.08
Eye Diameter	4.56 ± 0.05	4.37 ± 0.04*#	5.06 ± 0.08*	4.48 ± 0.04
Head Length	13.36 ± 0.10	13.68 ± 0.10*	13.40 ± 0.14	13.12 ± 0.12
Predorsal Length	24.05 ± 0.15	23.62 ± 0.18#	25.50 ± 0.22*	22.13 ± 0.15*
Head Depth	12.63 ± 0.16	14.27 ± 0.13*#	11.37 ± 0.20*	12.90 ± 0.17
Body Depth	14.92 ± 0.15	16.48 ± 0.16*#	13.49 ± 0.31*	14.10 ± 0.19*

plasticity, or the effect of random genetic drift. Traits that contributed strongly to discrimination among clades in McGuigan et al.'s (2000) study (i.e. those with strong phylogenetie signal) showed the greatest differences among species in this study, strongly supporting the species status of *M. utcheensis*. Additionally, all populations included in the morphological analyses came from similar habitats (fast flowing streams in closed forest), reducing the possibility that observed differences are due to local adaptation, or phenotypic plasticity.

As doeumented above, historically there has been considerable confusion over species assignments in the Wet Tropics. In this study, all 3 species of the region are distinct in morphology. However, the differences between them are not pronouneed and the level of variation within speeies suggests that none of the traits are diagnostic (Tables 2 and 3). Allen & Cross (1982) described *M. eachamensis* and indicated that it differs from *M. s. splendida* in a number of traits, including having a consistently shallower body. The opposite was observed in this study, with *M. eachamensis* being consistently deeper in the body than *M. s. splendida* (Table 2). Given the evidence of a long-term lack of gene flow (McGuigan et al., 2000), the morphological divergence between species is surprisingly limited. The lack of morphological specialisation of Australian freshwater fish has been noted previously (MeDowall, 1981), and similarity of rainbowfish in the Wet Tropics may be a related phenomenon. Despite the inconvenience such an approach would cause, I recommend that assignment of fish to species be based on multivariate morphological analyses of multiple populations, preferrably with supporting molecular data (see Zhu et al., 1998).

DISTRIBUTION AND HABITAT. *Melanotaenia utcheensis* was discovered through thc identification of a unique mtDNA lineage, more closely related to southern species than to other north Queensland species (McGuigan et al., 2000: fig. 1). The above analyses confirmed *M. utcheensis* as a discrete speeies by demonstrating that the unique mtDNA lineage correlates with a unique morphology. Morphological data for north Queensland rainbowfish is limited, such that the distribution of *M. utcheensis* might be better determined through examination of the distribution of mtDNA lineages (McGuigan & Moritz, unpubl. data; Fig. 1).

The *M. utcheensis* mtDNA lineage has been observed allopatrieally in a tributary of the lower South Johnstone River (Utehee Creek) and in lower (Fisher and Rankin Creeks) and upper (Short Creek and an unnamed creek near Malanda) tributaries of the North Johnstone R (McGuigan & Moritz, unpubl. data; Fig. 2). The *M. utcheensis* mtDNA lineage was also observed

TABLE 3. The percentage of the surveyed fish that are observed to have each values of the meristic traits vertical scale rows, pectoral fin rays, first dorsal spines and second dorsal and anal soft fin rays. These traits are those observed to differ among species (Table 2).

Species	Vertical Scale Rows							Pectoral Rays					
	29	30	31	32	33	34	35	10	11	12	13	14	15
utcheensis	2	47	8	4	9	21	9		6	53	24	8	9
eachamensis	7	13	27	24	19	9	1	1	29	49	21		
splendida				28	44	28			16	68	16		
duboulayi			12	25	28	25	10	7	40	50	3		
Species	First Dorsal Fin Spines							Second Dorsal Soft Rays					
	2	4	5	6	7	5	9	10	11	12	13	14	15
utcheensis		8	55	28	9			36	49	15			
eachamensis		11	41	42	6			8	33	29	26	2	2
splendida		24	64	12			4	40	36	20			
duboulayi	3	17	60	20		2	3	15	28	30	20	2	
Species	Soft Anal Fin Rays												
	16	17	18	19	20	21	22	23					
utcheensis		8	30	45	9	8							
eachamensis	8	7	28	26	25	3	3						
splendida			8	16	40	32		4					
duboulayi		12	33	30	20	5							

at several sites in the main channel, upland (Ithica, Gillies and Williams Creeks) and lowland (Tregothanana) tributaries of the North Johnstone R (Fig. 2), admixed at various proportions with *M. s. splendida* mtDNA (Zhu et al., 1998; McGuigan & Moritz, unpubl. data). *Melanotaenia utcheensis* co-occurs, at a low frequency, with the more common *M. eachamensis* mtDNA lineage at one site, Bromfield Swamp, the headwaters of the North Johnstone River (McGuigan & Moritz, unpubl. data).

The South Johnstone River has been surveyed extensively, making it unlikely there are undiscovered populations in this drainage. However, the *M. utcheensis* lineage in so many sites in the North Johnstone River, along with the many unsampled tributaries, raises the possibility of undiscovered populations in that catchment.

Analyses of mtDNA sequence suggest that, while *M. utcheensis* and *M. eachamensis* are old species that evolved in situ, *M. s. splendida* is a young species and has colonised the region recently (McGuigan et al., 2000; Hurwood & Hughes, 2001). It is not yet clear whether the admixture of mtDNA lineages in the North Johnstone River is the due to the occurrence of *M. utcheensis* and *M. s. splendida* in sympatry, or to either current or historical hybridisation. The co-occurrence of *M. eachamensis* and *M. utcheensis* at only one site, despite frequent co-occurrence of each with *M. s. splendida*, suggests the old endemics are characterised by barriers to dispersal and gene flow; lack of geographic discontinuity suggest the barriers may be ecological. If *M. utcheensis* and *M. s. splendida* evolved allopatrically, only recently coming into contact, they may not have evolved any mechanisms that would prevent hybridisation. Freshwater fish show unusually high levels of hybridisation and introgression (Turner, 1999). A documented threat to the conservation of freshwater fish is loss of genetic identity through introgressive hybridisation with introduced taxa (Berrebi, 1997). In many cases hybridisation is facilitated by modification of habitat and human-mediated species introductions; conditions that are met in N Qld.

Within *M. utcheensis* there are 2 MtDNA lineages, 1 on the Atherton Tablelands (e.g., Short Creek) and 1 primarily in the lowlands (e.g., Utchee Creek) (McGuigan et al., 2000: fig. 1). The presence of these sister lineages with a highly structured geographic distribution suggests long-term barriers to gene flow, and considerable antiquity of the endemic lineage. With additional information on ecology and interactions of rainbowfish in the Wet Tropics, it may become appropriate to accord species status to these 2 lineages, which are differentiated morphologically (McGuigan, unpubl. data). Lacking

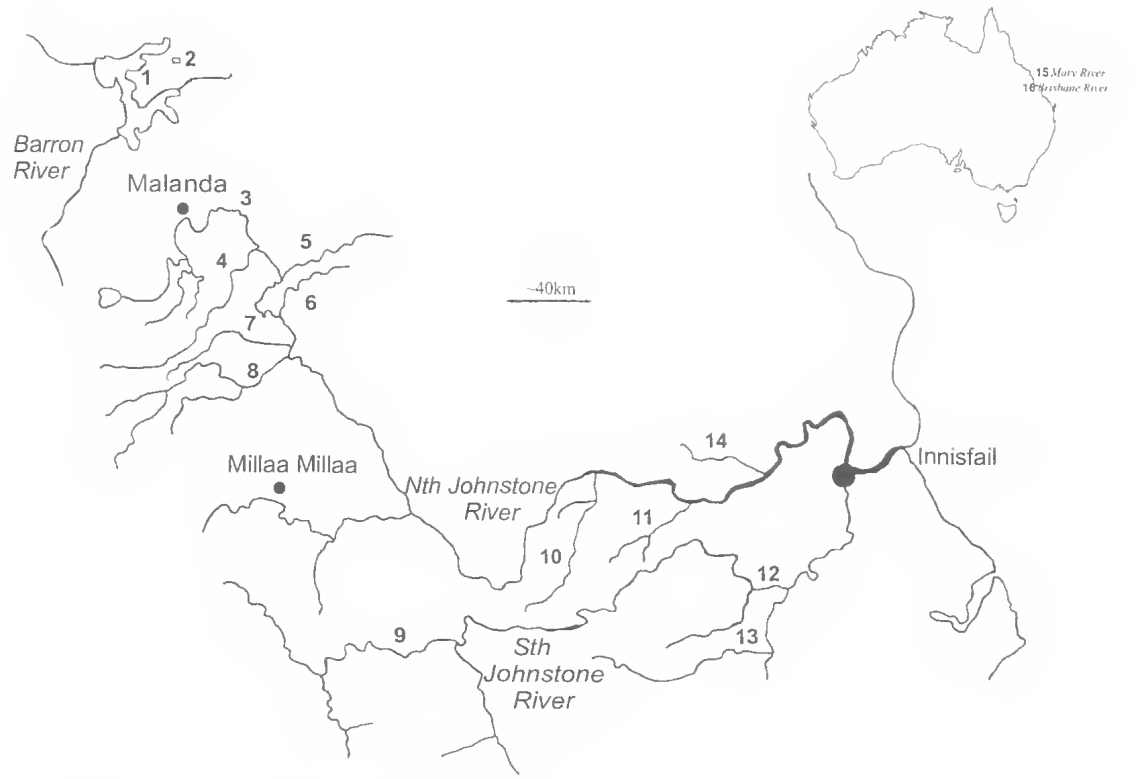

FIG. 2. Distribution of *Melanotaenia* species as determined from the distribution of mtDNA lineages (McGuigan & Moritz, unpubl. data). Sites sampled in this study indicated with *: 1, Tinaroo Dam (*M. s. splendida*: 17°09'30"S 145°35'10"E); 2, Lake Euramoo (*M. eachamensis*: 17°09'30"S 145°37'40"E); 3, Upper North Johnstone R. (*M. s. splendida*: 17°30'30"S 145°37'20"E); 4, Ithica R. (*M. utcheensis*: 17°24'25"S 145°37'10"E); 5, * Short Ck (*M. utcheensis*: 17°23'00"S 145°40'00"E); 6, unnamed tributary (*M. utcheensis*: 17°23'50"S 145°39'20"E); 7, Gillies Ck (*M. utcheensis*: 17°25'40"S 145°36'15"E); 8, * Dirran Ck (*M. eachamensis*: 17°28'30"S 145°32'53"E); 9, * Upper South Johnstone R. (*M. eachamensis*: 17°39'25"S 145°42'55"E); 10, Rankin Ck (*M. utcheensis*: 17°34'15"S 145°53'55"E); 11, * Fisher Ck (*M. utcheensis*: 17°34'55"S 145°53'55"E); 12, * Lower South Johnstone R. (*M. s. splendida*: 17°43'50"S 145°56'00"E); 13, * Utchee Ck (*M. utcheensis*: 17°38'30"S 145°56'20"E); 14, Tregothanana Ck (*M. utcheensis*: 17°31'20"S 145°57'30"E); 15, * Amamoor Ck (*M. duboulayi*: 26°21'S 152°40`E) and; 16, * Kholo Ck (*M. duboulayi*).

such data, I have taken the conservative approach of recognising both lineages as a single species.

Melanotaenia utcheensis is found in moderate to fast flowing water, in sections of stream consisting of deep pools separated by short runs. The substrate consists of cobbles and boulders with little fine sediment. Most sites have good visibility, but Rankin Creek and the lower North Johnstone main channel have very poor visibility due to large amounts of suspended solids. Visibility varies substantially across time, probably due to seasonal changes in land use and rainfall. Utchee Creek is the most structurally complex site with exposed root masses and overhanging vegetation. Other sites have undercut banks or grass beds. Sampled sites in Fisher, Utchee and Ithica Creeks have a riparian buffer zone dominated by native vegetation. Other sites have highly disturbed riparian vegetation (completely absent or dominated by exotic species). These sites are located in agricultural lands such as banana and tea plantations.

Melanotaenia utcheensis commonly co-occurs with purple spotted gudgeons (*Mogurnda adspersa*), long finned eels (*Anguilla reinhardtii*) and less commonly with blue-eyes (*Psuedomugil signifer*), roman nosed gobbies (*Awaous acritosis*), swamp eels (*Ophisternon* sp.), grunters (*Hephaestus* sp.) and exotic guppies (*Poecilia reticulata*) (pers. obs.; B. Pusey, pers. comm.).

The Wet Tropics of north Queensland are listed

FIG. 3. *Melanotaenia utcheensis*, ♂, Utchee Creek, South Johnstone R., northeast Queensland.

as a World Heritage area, partly in recognition of the high level of endemism. As yet, there is little known about this most recent addition to the endemic fauna, *M. utcheensis*. The geographic separation of populations of *M. eachamensis* and *M. utcheensis*, and the structure of genetic diversity within the latter, suggest a distribution that has been stable over a long period. It is not yet clear what the mixed populations of *M. s. splendida* and *M. utcheensis* represent. Pure *M. utcheensis* populations are currently known from only five sites (Fig. 2), with stream structure suggesting a restricted area of occupancy at those sites. Observations on population size during sampling suggested that population size was fewer than 1,000 mature individuals per site. If the mixed populations of *M. s. splendida* and *M. utcheensis* represent different stages in an ongoing exclusion of *M. utcheensis* through competition, predation or introgressive hybridisation, *M. utcheensis* would qualify as vulnerable under the criteria of the World Conservation Union. *M. eachamensis* is infamous as the first Australian freshwater fish to be declared extinct (in the wild). Although it has been rediscovered in the wild (Zhu et al., 1998), its disappearance from Lake Eacham is a strong warning for management of freshwater fish. Circumstantial evidence suggests that the cause of the demise of *M. eachamensis* in Lake Eacham was the introduction of 4 non-endemic piscivorous species (Barlow et al., 1987). In addition to the threat of predation, the potential for loss of genetic identity through hybridisation, at the population and species levels, should be considered in formulation of management strategies. Translocation of fish, either deliberately, or accidentally as a by-product of general water movement, or as live bait for fishing, has the potential to impact severely on diversity.

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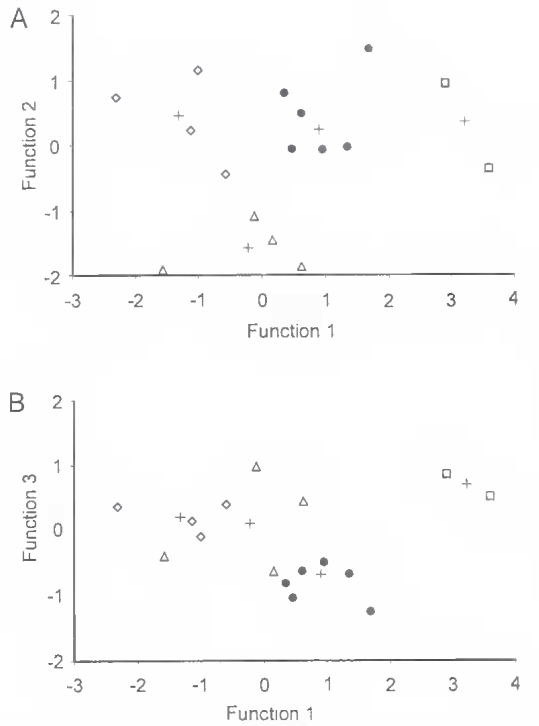

FIG. 4. Mean score for ♂s and ♀s of each population on: A, functions 1 and 2; and B, functions 1 and 3 of the Discriminant Functions Analysis. (◊ *M. eachamensis*, □ *M. s. splendida*, Δ *M. duboulayi*, ● *M. utcheensis*, + group centroids.

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